

SEQUENCE LISTING

<110> Dale, James B.

<120> GROUP A STREPTOCOCCAL VACCINES

<130> 481112.410

<140> US 09/151,409

<141> 1998-09-10

<150> US 60/058,635

<161> 1997-09-12

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 24 M protein DNA

<400> 1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 24 M protein DNA

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<212> DNA

<213> Artificial Sequence

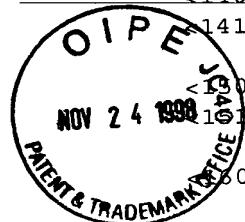
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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 5 M protein DNA

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<210> 4
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<212> DNA
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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 5 M protein DNA

<400> 4 30
gggggggtcg acctcagttt ttaacccttc

<210> 5
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<212> DNA
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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 6 M protein DNA

<400> 5 30
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<210> 6
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 6 M protein DNA

<400> 6 30
ggggggccat ggtaacttgt cattatttagc

<210> 7
<211> 30
<212> DNA
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Synthesis -- Primer, hybridizes to streptococcal
type 19 M protein DNA

<400> 7 30
ggggggccat ggagagtgcg ttataactagg

<210> 8
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<212> DNA
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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 19 M protein DNA

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<210> 9
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<213> Artificial Sequence

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Synthesis -- Primer, hybridizes to streptococcal
type 1 M protein DNA

<400> 9 30
ggggggctgc agaacggta tggtaatcct

<210> 10
<211> 30
<212> DNA
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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 1 M protein DNA

<400> 10 30
ggggggggta ccagctctct taaaatctct

<210> 11
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 3 M protein DNA

<400> 11 30
ggggggggta cttgttaga tcaggttaca

<210> 12
<211> 30

<212> DNA
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<220>
<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 3 M protein DNA

<400> 12 30
ggggggatcg atatttaact cttgtaacag

<210> 13
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<212> DNA
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<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 24 M protein DNA

<400> 13 30
ggggggatcg atgtcgcgac taggtctcag

<210> 14
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Product of
Synthesis -- Primer, hybridizes to streptococcal
type 24 M protein DNA

<400> 14 33
ggggggaagc ttttacttac gtgcctctaa ttc

<210> 15
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<212> DNA
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<223> Description of Artificial Sequence: Hexavalent M
fusion gene sequence constructed from
streptococcal type 24, 5, 6, 19, 1 and 3 M protein
DNAs

<220>
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<222> (1)..(1149)

<400> 15 48
gca tgc atg gtc gcg act agg tct cag aca gat act ctg gaa aaa gta
Ala Cys Met Val Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val

1	5	10	15	
caa gaa cgt gct gac aag ttt gag ata gaa aac aat acg tta aaa ctt Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu 20		25	30	96
aag aat agt gac tta agt ttt aat aat aaa gcg tta aaa gat cat aat Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn 35	40	45		144
gat gag tta act gaa gag ttg agt aat gct aaa gag aaa cta cgt gga Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly 50	55	60		192
tcc gcc gtg act agg ggt aca ata aat gac ccg caa aga gca aaa gaa Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu 65	70	75	80	240
gct ctt gac aag tat gag cta gaa aac cat gac tta aaa act aag aat Ala Leu Asp Lys Tyr Glu Leu Glu Asn His Asp Leu Lys Thr Lys Asn 85	90	95		288
gaa ggg tta aaa act gag aat gaa ggg tta aaa act gag aat gaa ggg Glu Gly Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Asn Glu Gly 100	105	110		336
tta aaa act gag aat gaa ggg tta aaa act gag gtc gac aga gtg ttt Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Val Asp Arg Val Phe 115	120	125		384
cct agg ggg acg gta gaa aac ccg gac aaa gca cga gaa ctt ctt aac Pro Arg Gly Thr Val Glu Asn Pro Asp Lys Ala Arg Glu Leu Leu Asn 130	135	140		432
aag tat gac gta gag aac tct atg tta caa gct aat aat gac aag tta Lys Tyr Asp Val Glu Asn Ser Met Leu Gln Ala Asn Asn Asp Lys Leu 145	150	155	160	480
cca tgg aga gtg cgt tat act agg cat acg cca gaa gat aag cta aaa Pro Trp Arg Val Arg Tyr Thr Arg His Thr Pro Glu Asp Lys Leu Lys 165	170	175		528
aaa att att gac gat ctt gac gca aaa gaa cat gaa tta caa caa cag Lys Ile Ile Asp Asp Leu Asp Ala Lys Glu His Glu Leu Gln Gln 180	185	190		576
aat gag aag tta tct ctg cag aac ggt gat ggt aat cct agg gaa gtt Asn Glu Lys Leu Ser Leu Gln Asn Gly Asp Gly Asn Pro Arg Glu Val 195	200	205		624
ata gaa gat ctt gca gca aac aat ccc gca ata caa aat ata cgt tta Ile Glu Asp Leu Ala Ala Asn Asn Pro Ala Ile Gln Asn Ile Arg Leu 210	215	220		672
cgt cac gaa aac aag gac tta aaa gcg aga tta gag aat gca atg gaa Arg His Glu Asn Lys Asp Leu Lys Ala Arg Leu Glu Asn Ala Met Glu 225	230	235	240	720

gtt gca gga aga gat ttt aag aga gct ggt acc ttg tta gat cag gtt	768
Val Ala Gly Arg Asp Phe Lys Arg Ala Gly Thr Leu Leu Asp Gln Val	
245	250
255	
aca caa tta tat act aaa cat aat agt aat tac caa caa tat aat gca	816
Thr Gln Leu Tyr Thr Lys His Asn Ser Asn Tyr Gln Gln Tyr Asn Ala	
260	265
270	
caa gct ggc aga ctt gac ctg aga caa aag gct gaa tat cta aaa ggc	864
Gln Ala Gly Arg Leu Asp Leu Arg Gln Lys Ala Glu Tyr Leu Lys Gly	
275	280
285	
ctt aat gat tgg gct gag agg ctg tta caa gag tta aat atc gat gtc	912
Leu Asn Asp Trp Ala Glu Arg Leu Leu Gln Glu Leu Asn Ile Asp Val	
290	295
300	
gcg act agg tct cag aca gat act ctg gaa aaa gta caa gaa cgt gct	960
Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val Gln Glu Arg Ala	
305	310
320	
gac aag ttt gag ata gaa aac aat acg tta aaa ctt aag aat agt gac	1008
Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu Lys Asn Ser Asp	
325	330
335	
tta agt ttt aat aat aaa gcg tta aaa gat cat aat gat gag tta act	1056
Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn Asp Glu Leu Thr	
340	345
350	
gaa gag ttg agt aat gct aaa gag aaa cta cgt aaa aat gat aaa tca	1104
Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Lys Asn Asp Lys Ser	
355	360
365	
cta tct gaa aaa gct agt aaa att caa gaa tta gag gca cgt aag	1149
Leu Ser Glu Lys Ala Ser Lys Ile Gln Glu Leu Glu Ala Arg Lys	
370	375
380	
taaaaagctt	1158

<210> 16
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<400> 16
 Ala Cys Met Val Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val
 1 5 10 15

Gln Glu Arg Ala Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu
 20 25 30

Lys Asn Ser Asp Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn
 35 40 45

Asp Glu Leu Thr Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Gly
 50 55 60

Ser Ala Val Thr Arg Gly Thr Ile Asn Asp Pro Gln Arg Ala Lys Glu

65

70

75

80

Ala Leu Asp Lys Tyr Glu Leu Glu Asn His Asp Leu Lys Thr Lys Asn
85 90 95

Glu Gly Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Asn Glu Gly
100 105 110

Leu Lys Thr Glu Asn Glu Gly Leu Lys Thr Glu Val Asp Arg Val Phe
115 120 125

Pro Arg Gly Thr Val Glu Asn Pro Asp Lys Ala Arg Glu Leu Leu Asn
130 135 140

Lys Tyr Asp Val Glu Asn Ser Met Leu Gln Ala Asn Asn Asp Lys Leu
145 150 155 160

Pro Trp Arg Val Arg Tyr Thr Arg His Thr Pro Glu Asp Lys Leu Lys
165 170 175

Lys Ile Ile Asp Asp Leu Asp Ala Lys Glu His Glu Leu Gln Gln Gln
180 185 190

Asn Glu Lys Leu Ser Leu Gln Asn Gly Asp Gly Asn Pro Arg Glu Val
195 200 205

Ile Glu Asp Leu Ala Ala Asn Asn Pro Ala Ile Gln Asn Ile Arg Leu
210 215 220

Arg His Glu Asn Lys Asp Leu Lys Ala Arg Leu Glu Asn Ala Met Glu
225 230 235 240

Val Ala Gly Arg Asp Phe Lys Arg Ala Gly Thr Leu Leu Asp Gln Val
245 250 255

Thr Gln Leu Tyr Thr Lys His Asn Ser Asn Tyr Gln Gln Tyr Asn Ala
260 265 270

Gln Ala Gly Arg Leu Asp Leu Arg Gln Lys Ala Glu Tyr Leu Lys Gly
275 280 285

Leu Asn Asp Trp Ala Glu Arg Leu Leu Gln Glu Leu Asn Ile Asp Val
290 295 300

Ala Thr Arg Ser Gln Thr Asp Thr Leu Glu Lys Val Gln Glu Arg Ala
305 310 315 320

Asp Lys Phe Glu Ile Glu Asn Asn Thr Leu Lys Leu Lys Asn Ser Asp
325 330 335

Leu Ser Phe Asn Asn Lys Ala Leu Lys Asp His Asn Asp Glu Leu Thr
340 345 350

Glu Glu Leu Ser Asn Ala Lys Glu Lys Leu Arg Lys Asn Asp Lys Ser
355 360 365

Leu Ser Glu Lys Ala Ser Lys Ile Gln Glu Leu Glu Ala Arg Lys
370 375 380